

EXHIBIT A

Alignment of amino acid sequences of glutaminases

		1		50
gls (2247)	(1)	MVAFESLWPQNLSCTRVYSAKEI	ELDSMLTMIPEYLHEILDDVRDTTS	
GLSA_CORGL	(1)	-----	-----	
GLSA_COREF	(1)	-----	MTTHPLIMPIPEYFEELLESVRSDVS	
GLSA1_BRAJA	(1)	-----	PPPPASAWTRSKP-PRLRFLDTCNEFSAEIS	
GLSA2_BRAJA	(1)	-----	MDTQPIRLPSIAGATRSAAGYPTRP-PERRFLDCHEFRGDSS	
GLSA_ANASP	(1)	-----	DQANQDLETRPSPLKVNTHSKYSLKE	
Consensus	(1)	MS	SA	MLTMIPIPEYL ETDDVRSDTS
		51		100
gls (2247)	(51)	GELADYIPELKSAADPNPLAVALCTVIGHIYSAGDDDIETMQSISKPFAY		
GLSA_CORGL	(23)	GELADYIPELKSAADPNPLAVALCTVIGHIYSAGDDDIETMQSISKPFAY		
GLSA_COREF	(27)	GEVAQYIPQLKADDPNPLAAMCTVDGHIYGAGDDEHETMQSISKPFAY		
GLSA1_BRAJA	(33)	GAVADYIPELGNADPAYFGISLATEQGHVYEVGDSRVPFTIQSISKPFV		
GLSA2_BRAJA	(43)	GELADYIPELKRNADPHFGIALVTUDGHVYEVGDSAVPFTIQSVSKAFV		
GLSA_ANASP	(34)	GIVANYIPELAKVNPDLFSISIVTVDGQVYQVGDYQQLFTIQSISKVFAY		
Consensus	(51)	GELADYIPELK ADPNPLAVALCTVDGHTY VGDDDIETIQSISKPFAY		
		101		150
gls (2247)	(101)	ALALQE CGFDEVASASVALEPSGEAFNEISLDG-ENRPMNPMINAGAIAIN		
GLSA_CORGL	(73)	ALALQE CGFDEVASASVALEPSGEAFNEISLDG-ENRPMNPMINAGAIAIN		
GLSA_COREF	(77)	ALALQE CGPEKVFATIVGLEPSGEAFNEISLDGNTNRPMPMNNAGAIAVN		
GLSA1_BRAJA	(83)	ALALDLGAGRVSEATGVEPSGDPFNSIRLNSDN-EPENPMVNAGAIACT		
GLSA2_BRAJA	(93)	ALALETVGEERVSATIGVEPSGEAFNSRLTNDN-RPENPMVNAGAIACS		
GLSA_ANASP	(84)	GEALEDHGROYLTVRGVEPTGEAFNAIEDEQSKRPNPMVNAGAIATT		
Consensus	(101)	ALALQE G DRVSASVGLEPSGEAFNEISLDG NRPMPNPMINAGAIAIN		
		151		200
gls (2247)	(150)	QLINGSDSTIVEDRVEKIRHYSELAGRELITDRVIAESELAGADRNL SIA		
GLSA_CORGL	(122)	QLINGSDSTIVEDRVEKIRHYSELAGRELITDRVIAESELAGADRNL SIA		
GLSA_COREF	(127)	QLINGSSESSVEDRVEKIRSYFSALAGRELNDRQSETEIEGADRNL SIA		
GLSA1_BRAJA	(132)	GLYDSDKG-AEAPEQIRLALSRSFAGRDLAVDEAVYSESQTGDRNRAT		
GLSA2_BRAJA	(142)	GLYEVDG-KGAFERVRSKLSEFARELGVDEAVHASEIATGDRNRAT		
GLSA_ANASP	(134)	SLLKGACAA-TERINRVLLEMERRYIHDVFDLISVFTSERSTGHRNRAMA		
Consensus	(151)	QLINGSDSTVEDRVEKIR YFSELAGREL TDRVIAESELATADRNRAT		
		201		250
gls (2247)	(200)	HHLRNYGVIEDEAHDAVLSYTLOCATKVTIRDALAVMTATLAAGGTIPITG		
GLSA_CORGL	(172)	HHLRNYGVIEDEAHDAVLSYTLOCATKVTIRDALAVMTATLAAGGTIPITG		
GLSA_COREF	(177)	HHLRNYGVIEDDAHDAVLSYTLOCATKVTARDALAVMTATLAAGGTIPITG		
GLSA1_BRAJA	(180)	YLLKINAVISDVAVAEDVVYFRCATLVTARDALAVMTATLANRGVINPV		
GLSA2_BRAJA	(190)	WLRNVAEPDDDAVDALEDDVVYFRCATLVTARDALAVMTATLANRGVINPV		
GLSA_ANASP	(182)	HLMLNFGMIDRNIEEADLYFQQCAMVNCHDLAVMAATLANRGVINPV		
Consensus	(201)	HLLRNYGVIEDDAHDAVLSYTLOCATKVTARDALAVMTATLANRGTPITG		
		251		300
gls (2247)	(250)	KKLTDARVCRLTLSVMASAGMYDEAGQWLTSTVGIPAKSGVAGGLJGILPG		
GLSA_CORGL	(222)	KKLTDARVCRLTLSVMASAGMYDEAGQWLTSTVGIPAKSGVAGGLJGILPG		
GLSA_COREF	(227)	EKLVDARVARLVLSTMASAGMYDEAGQWLTATVGLIPAKSGVSGGLVGVLPG		
GLSA1_BRAJA	(230)	EDVMSAVAIISRLTLSVMTSSGMYDVAGEWYRIGIPAKSGVGGGIEALPA		
GLSA2_BRAJA	(240)	AQVITPHIVARTTLSVMTSSGMYDVAGEWTYRGIPAKSGVGGGIEALPS		
GLSA_ANASP	(232)	EQAVNSRTIKDILSVMYTCCMYNAGEWAKVGLIPAKSGVCGGIHAVPN		
Consensus	(251)	EQLLDARVIRTLTLSVMASAGMYDEAGQWLYTVGIPAKSGVAGGIITAIPPG		
		301		350
gls (2247)	(300)	QLGIATFSPRLNPKGSNSVRGVKIFKALSDDMGLHLMSIEVSGHAVRSIT		
GLSA_CORGL	(272)	QLGIATFSPRLNPKGSNSVRGVKIFKALSDDMGLHLMSIEVSGHAVRSIT		
GLSA_COREF	(277)	QLGIATFSPRLNSQGPVRGVIEFKALSEDMDGLHLMSAEIETQHAVAIE		
GLSA1_BRAJA	(280)	REGLGGSYSPKLDKHGNNSVRGKVKVCEALSSHDLHMRNRSDDARNAVIADY		
GLSA2_BRAJA	(290)	QLGLGTFSPLLDNHFNNSVRGLKVCEALSAFDLHMRNRADVRTSVMADY		
GLSA_ANASP	(282)	LMGIAVESPPLDRGNSNSVRGVKVKCEELSQQEGLHLFECMKVNGENGVGN		
Consensus	(301)	QLGIATFSPRLN KGNSNSVRGVKIFKALSDDMGLHLMS E VS HAVRAI		
		351		400
gls (2247)	(350)	RDG-----DTTFOOMQAMNFSASESELHAIIVEH		
GLSA_CORGL	(322)	RDG-----DTTFOOMQAMNFSASESELHAIIVEH		
GLSA_COREF	(327)	ERG-----DTTFOOMQAMNFSASESELHAIIVEH		
GLSA1_BRAJA	(330)	DIGKSPSRVRRRAQEREI LAAHEQEVRIELVGTLSLSAIDYVSRRAGR		

GLSA2_BRAJA	(340)	I YGISSRRSRQPHEQQILDERHS D IR N E V GAI N GT I DYVTRR T SE
GLSA_ANASP	(332)	C C
Consensus	(351)	DDG DTIIQLQGAMNFSASE FL I EH 401 450
gls(2247)	(379)	NFEGTEVVL D ITRVLSFH P VAIRMIKEGLKRIRDAGF E V F ILDPPDVLPD
GLSA_CORGL	(351)	NFEGTEVVL D ITRVLSFH P VAIRMIKEGLKRIRDAGF E V F ILDPPDVLPD
GLSA_COREF	(356)	DFTGEKVVLDI S RVP M FRP M GRR L YKEGLRRIRDNGE K VAIYDPE D ILPD
GLSA1_BRAJA	(380)	P-RPQFV H FDL T RTS T TRAGARL V CAFE E AA N NT V ESGVRRASKE
GLSA2_BRAJA	(390)	PPNAPL E EDFRRVPDITAAGAE E GET T TAEGNAVTTIESGLE E ASAV
GLSA_ANASP	(335)	
Consensus	(401)	F G VVLDL T RV SF PVG R L IKEGLKRIRDAGF V I DPDDVLPD 451 500
gls(2247)	(429)	FMFSDGTICKERV
GLSA_CORGL	(401)	FMFSDGTICKERV
GLSA_COREF	(406)	FDFSDGT K SPQVDDPEEL
GLSA1_BRAJA	(429)	WNTLREWTAELLNVRDFYLLDTAEWAEDQIVYRYGGSIDFHETTELAEQ
GLSA2_BRAJA	(440)	WAAIAARTGDP R RLRRFALLDDAEWAEDQVIYRGFFTDVKESVHLGEQ
GLSA_ANASP	(335)	
Consensus	(451)	F FSDGT R 501 550
gls(2247)	(442)	
GLSA_CORGL	(414)	
GLSA_COREF	(424)	
GLSA1_BRAJA	(479)	PLLEG L SADELAELGAICTIRTYQSGAKIL T TD G PA D ALFFL R SGAVHVT
GLSA2_BRAJA	(490)	ALLAELDTDEIAAVKLSTTRHYTAGQRVIAAGAPANSLFF L OSGMVS V K
GLSA_ANASP	(335)	
Consensus	(501)	551 600
gls(2247)	(442)	
GLSA_CORGL	(414)	
GLSA_COREF	(424)	
GLSA1_BRAJA	(529)	LPDGVR L ATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR
GLSA2_BRAJA	(540)	LRSGVRLASLGPGMEFGEMAILERTRSADVFA D TPVAC L PLDSFADYR
GLSA_ANASP	(335)	
Consensus	(551)	
gls(2247)	(442)	601 635
GLSA_CORGL	(414)	
GLSA_COREF	(424)	
GLSA1_BRAJA	(579)	EQHPRASERIMRNLAQLLADRLIVANAKVDILTST
GLSA2_BRAJA	(590)	RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY
GLSA_ANASP	(335)	
Consensus	(601)	

GLSA_CORGL : Q8NMT3; *Corynebacterium glutamicum*
 GLSA_COREF : Q8FMX4; *Corynebacterium efficiens*.
 GLSA1_BRAJA : Q89NA7; *Bradyrhizobium japonicum*,
 GLSA2_BRAJA : Q89KV2; *Bradyrhizobium japonicum*
 GLSA_ANASP : QBYSZ5; *Anabaena* sp. (strain PCC 7120)

EXHIBIT B

Alignment of nucleotide sequences of glutamine synthetase genes

		1		50
2247	(1)	GTGGCGTTTGAA-ACCCCGGAAGAAAATGTCAAGTT		
13032	(1)	GTGGCGTTTGAA-ACCCCGGAAGAAAATGTCAAGTT		
CEFgInA1	(1)	GTGGCGTTTAAAC-ACCCCGGAAGAAATGTCAAGTT		
CEFgInA2	(1)	GTGGCCTCGAGCCGACAACCAACCCGGATGAGATCCTCAAGTT		
MtugInA2	(1)	ATGGACCAGACAGAAGGAAATTCTGTTCTCG		
MtugInA3	(1)	ATGACAGCCACACCCCTTGCCGCGGCCGCGAT		
MtugInA4	(1)	GTGACCGGCCCGGTTCGCCGCCGTTGGCTGGACCGAGTTGGAGGCACI		
MtugInA1	(1)	GTCACGGAAAAG-AGGCCCGACGACGCTTCAAACI		
Consensus	(1)	GTGGCGATGA ACCCCGGA GAA T GTCAAGTT		
		51		100
2247	(36)	CATCA-AGGATGAA-AACGTCGAGTTCGTGTACGTTCGATTACCG		
13032	(36)	CATCA-AGGATGAA-AACGTCGAGTTCGTGTACGTTCGATTACCG		
CEFgInA1	(36)	CATCA-AGGAUGAA-AACGTTGACTTCGTCGATGTCGATTCACCG		
CEFgInA2	(45)	CATCC-CGGACAAAT-GACATCACTGGGTGACCGTCCAGTTCACCG		
MtugInA2	(30)	TACCC-TGGAAGAACCGCAGACATCGGTTTCGTCGCGCTGTGGTTACAG		
MtugInA3	(33)	CGCCAATTGGAGGCAGAGGCCGTCGACACCGTCATCGGACCGTCTGA		
MtugInA4	(51)	GTCG-CGGCCGGT-GACGTCGACACCGTCATCGTCGCGTTACCG		
MtugInA1	(36)	TGCCA-AGGACGAG-AAGTCGAATAATGTCGACGTCGGTTCTGTG		
Consensus	(51)	CATCA AGGA GAA GACGTCGACTTCGTCGACGTCCGGTTACCG		
		101		150
2247	(80)	ACCTTCCCGCACCGAGCAGCACTTCAGCATCCAGCTGCCAGCTTCGAT		
13032	(80)	ACCTTCCCGCACCGAGCAGCACTTCAGCATCCAGCTGCCAGCTTCGAT		
CEFgInA1	(80)	ACCTTCCCGGAATCGAGCAGCACTTCAGCATCCCGCACTCGCTCTGAT		
CEFgInA2	(89)	ACCTTCCCGCACCGAACAGCACCTGTCGCGCCATCGGCCAGCGAACCTGCA-		
MtugInA2	(77)	ACGTGCTCGGTTTCCTCAAGTCGGTCGCCATCGGCCAGCGAACCTGCA-		
MtugInA3	(83)	ACCCCGCCGGACTCACCCAGGCCAAGACCGTGCAGATACCGCGGACCAA-		
MtugInA4	(95)	ACATGCGAGGGC-CGGCTGGCCGAAACGGATATCGGGGGCGCA-		
MtugInA1	(80)	ACCTGCTGGCATCATGCGAGCACTTCACGATTCCGGCTTCGGCTTGAC		
Consensus	(101)	ACCTTCCCGCATCGAGCAGCACTTCAGCATCCC GCAGCGGCTTCGA		
		151		200
2247	(130)	GCAGATAACAGTCGAAGAAGGTCICGCATTCGACGGATCCCTGATCCGG		
13032	(130)	GCAGATAACATCGAAAGAAGGTCICGCATTCGACGGATCCCTGATCCGG		
CEFgInA1	(130)	GAGGACGGCATCGAGGAAGGCCCTCGCCTTCGACGGTTCCTCATCCGG		
CEFgInA2	(139)	GAATCCGGCATGGAAAACCGGACTGGCCTTCGACGGGTCATCGATCACGG		
MtugInA2	(126)	GGGCGCCTTCGAGGAAGGCATCGGCCTCGACGGATCCCTGATCGAGGG		
MtugInA3	(132)	CAATTCGCCAA-TCTTGGCTCGGCCAGTCGGGTTGCGCA-		
MtugInA4	(138)	-T-TCGTCGACGACATAGCCACCCGCCGCTGAGGTGCTTCAG		
MtugInA1	(130)	AAGAGCGTGTGGACGACGGCTGGCCTTGTGGCTTCGACGGTCGATTCCGG		
Consensus	(151)	G G CGC TTCGA GA GGCTCGCCTTCGACGG TCCTGATCCGG		
		201		250
2247	(180)	CTTCACCAAGCATCGACGAATCTGACATGAATCTCCCTGCCAGACCTC-GGA		
13032	(180)	CTTCACCAAGCATCGACGAATCTGACATGAATCTCCCTGCCAGACCTC-GGA		
CEFgInA1	(180)	TTTCAACCACTTGAATGAATCCGACATGAACCTGCTGCGCGATCTG-GCC		
CEFgInA2	(189)	ATACACCACTGTCGACGATTCGGACATGATGCTGCTGCCGATCTG-TCC		
MtugInA2	(174)	CTTTCGCGGGCTCGGAATCCGATACCGTGGCGACCCCGACCC		
MtugInA3	(174)	TACCTTCTGATCGACGAATGCAAGTATGCAATCACCGCAGACATCACTG		
MtugInA4	(180)	TATCTGCTGGCCGTTGGACGTCGACCTGAACACCGCTGCCCGCTAT-GCG		
MtugInA1	(180)	GTCAGTCGATCCACGAATCCGACATGTTGCTCTTCCGATCCCGAG		
Consensus	(201)	TTCACCAAGCATCGACGAATCCGACATGAATCGCTGCCAGACCTC G		
		251		300

2247	(229)	ACGGCCACCCCTTGATCC	AATCCGCA	GGCAAAGACCCCTGAACGT			
13032	(229)	ACGGCCACCCCTTGATCC	AATCCGCA	GGCAAAGACCCCTGAACGT			
CEFgInA1	(229)	ACCGCGAAGATCGA	CC	GTCGCA	GGCGAAGACCCCTGAACGT		
CEFgInA2	(238)	ACGGCGTTCATCGACCC	GTTCCGCA	GTCGAAAGACCCCTGAACGT			
MtugInA2	(218)	-CGTCGACCTTCCAGGT	GCTGCCCTG	GGCCA	CC		
MtugInA3	(224)	TGGTCGGCGATCAACGT	CTCCGCAT	CGA	TC		
MtugInA4	(229)	ATGGCCAGTTGGACACCCG	GTACGGCATA	GGTGA	TGACGGCCGACTT		
MtugInA1	(229)	ACGGCGCGCATCGACCC	GTTCCGCGC	GGCCA	AAAGACCGCTGAATA		
Consensus	(251)	ACGGCGACCATCGACCC	GTTCCGCA	GGCGAAGACCCCTGAAC	T		
		301		350			
2247	(273)	-TAAGTTCTCGT	[CACGATCC]TTCACCCCG	GAGGC	TTCTCCCGCGAC		
13032	(273)	-TAAGTTCTCGT	[CACGATCC]TTCACCCCG	GAGGC	TTCTCCCGCGAC		
CEFgInA1	(273)	-CAAGTTCTCGTCCAT	GACCCCTTCAACCCG	GAGGC	TTCTCCCGCGAC		
CEFgInA2	(282)	-CAAGTTCTCGTCCAT	GACCCCTTCAACCCG	GAGGC	TTCTCCCGGGAT		
MtugInA2	(250)	-AGTIC	CGGCCACACCACT	CAGCGCGA	TGTTTGCGACATCA		
MtugInA3	(254)	-T	GTCCGCGTTCGGCAT	ATCGGGGACCGGG	TGGCGTIGGGCG		
MtugInA4	(279)	GTCCACTCTGGG	GTATTGGTACCGGG	AAACGGCGCTGGT	CATCG		
MtugInA1	(273)	-CAACTCTTTGTG	CACGACCCGTTACCCCT	GGAGGC	CGTACTCCCGCGAC		
Consensus	(301)	TAAGTTCTCGTCCACGACCCCTTCAACCGGGAGGC	GT	TCTCCCGCGAC	351	400	
2247	(322)	CCACCGAACGTTAGCACCGCAAGGCAGAGCAGTACCTGGC	A	CCACCGGG			
13032	(322)	CCACCGAACGTTGGCACGCAAGGCAGAGCAGTACCTGGC	A	CCACCGGG			
CEFgInA1	(322)	CCCCGCAATGTGGCACGT	AAGGCCGAGCAGT	CCCTGGC	CTCCACCGG		
CEFgInA2	(331)	CCCCGCAACATCGCCCGCAAGGCAGAGGAGTACCTGGC	A	TTCCACCGG			
MtugInA2	(293)	CCATGGCGACGGCTCGG	-GTCTGGCGG	ACCCG	CGGCACGTG		
MtugInA3	(299)	CGGGGTCTTCGAGCAGGACGGCAACCGGT	CCCCG	CTGCAGCCG			
MtugInA4	(329)	CCGACCTGGTCTGGGCCAGGGCAGGGAGGT	CCCCG	TCTGGCGCGAGC			
MtugInA1	(322)	CCGCGAACATCGCCCGCAAGGCAGAGAAC	TACCTGAT	CAGCACTGG			
Consensus	(351)	CC CGAAC TGGC CGCAAGGCAGAGCAGTACCTGGC	CTGGCACCGG	401	450		
2247	(369)	CATTCGAGACACCTGCAACTTCGGCGCCGAGGC	TGAGTTCTACCTCTTCG				
13032	(369)	CATTCGAGACACCTGCAACTTCGGCGCCGAGGC	TGAGTTCTACCTCTTCG				
CEFgInA1	(369)	CATCGCCGACACCTGCAACTTCGGCGCCGAGGC	TGAGTTCTACCTCTTCG				
CEFgInA2	(378)	TTTCGCGGACACTGTAACTTCGGCGCCGAGGC	TGAGTTCTACATCTTCG				
MtugInA2	(337)	TTTCGCGGCGACCTG	ACGAAGGC	C-GGC	GA	ACTCGGC	TCTCCT
MtugInA3	(345)	AGGAAACTGAGCGGAT	CGAGGCCGCTTGCTGAT	GGCGG	GA	TGCGAC	
MtugInA4	(379)	ATTCTGCGCCGCTGAGCTCGATCGGAT	CAAGGC	CGCGGG	ACTGGTCG		
MtugInA1	(369)	CATCGCCGACACCGCAACTTCGGCGCCGAGGC	TGAGTTCTACATCTTCG				
Consensus	(401)	CATCGCCGACACCTGCAACTTCGGCGCCGAGGC	TGAGTTCTACCTCTTCG	451	500		
2247	(419)	ACTCCGTTCGCTACTCCACCGAGATGAA	CTCCGGCTCTACGA	GTAGAT			
13032	(419)	ACTCCGTTCGCTACTCCACCGAGATGAA	CTCCGGCTCTACGA	GTAGAT			
CEFgInA1	(419)	ACTCCGTTCGCTACTCCACCGAGATGAA	CTCCGGCTCTACGA	GTAGAT			
CEFgInA2	(428)	ACTCCGTGGGTCAGCTCCACCGAGATGAA	CTCCACGGAGGTGGAT				
MtugInA2	(380)	GCTACGCTGCACTCCGAAATCGAG	CTCTTCTCTGCTCAAG				
MtugInA3	(395)	CGGTAATCGGCCACGAAGTCGAA	CTCTCTCTGGTCGAC				
MtugInA4	(425)	CGGATGTGGCACCAGCTGGAGTCACTCGT	G-TTGGAC	ACCGGTAT			
MtugInA1	(419)	ATTCCGTGAGCTCGACTCGCGCCAAACGGCTCC	TCTACGAGGTGGAC				
Consensus	(451)	ACTCCGTGGCTACGACACCGAG TCAAC CCG	TTCTACGAGGTGGAT	501	550		
2247	(469)	ACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAA	ACCAACCTCGACGGAAC				

13032	(469)	ACCGAAGAAGGGCTGGTGGAACCGTGGCAAGGAACCAACCTCGACGGCAC				
CEFgInA1	(469)	ACCAACCGAGGGTTGGTGGAACCGTGGCGTGAGACCAACCTCGATGGCAC				
CEFgInA2	(478)	TCCGTGGAGGGCTGGTGGAACACGTGGTTCCCGGGAGAACCCCAGGGCAG				
MtugInA2	(418)	CCC-----GGACCCGAGGACGGG-----TCGGTCCCCG				
MtugInA3	(433)	GCGGA-C-G-GCCAGCGGCCGTGCCT-----TCGAGG-CIG				
MtugInA4	(472)	CGCC-AGGCA-TGGGCCAGCGG-GIA-----TCGGCGGCIG				
MtugInA1	(469)	GCCATCTGGGGTGGTGGAACACCGGGCGGGGACCGGAGGCCCGACGGCAG				
Consensus	(501)	CCGA GAGGGCTGGTGGAACCGTGGC GGA ACCAACCTCGACGGCAG				
	551	600				
2247	(519)	CCC AAACCTGGCGCAAAGAACCGGTCAAGGGGGCTACTTCCCAGTAG				
13032	(519)	CCCCAAACCTGGCGCAAAGAACCGGTCAAGGGGGCTACTTCCCAGTAG				
CEFgInA1	(519)	CCCCAAACCCGTTCCAAGAACCGGTCAAGGGGGCTACTTCCCAGTAG				
CEFgInA2	(528)	CAGGAACCTGGGTACAAGGTACGCCAGAAGGGGGTACTTCCCAGTAG				
MtugInA2	(446)	TCCC-GGTGCAAGGTAACGCCAGAAGGGGGTACTTCCCAGTAG				
MtugInA3	(463)	T-GGGC-GCAGTACGGGAGAAGGGGGTACTTCCCAGTAG				
MtugInA4	(505)	ACCC-CGCCAGCGA-CGAACTACGCCATAACGCCATAITGG				
MtugInA1	(519)	TCCCCAACCGGGGCTACAAGGTCCGCCACAAGGGGGGTAUTTCCCAGTAG				
Consensus	(551)	CCCCAACCGGGC AAG CGCG CAAGGGGGCTACTTCCCAGTAG				
	601	650				
2247	(569)	CA-CGATACGACCAAACCGTGGACGTGCGCGATGACATGGTTCGCAACC				
13032	(569)	CA-CGATACGACCAAACCGTGGACGTGCGCGATGACATGGTTCGCAACC				
CEFgInA1	(569)	CA-CCTACGACCAAGACCGTGGACGTGCGCGATGACATGGTTCGCAACC				
CEFgInA2	(578)	CA-CCTATGACCACTTCCAGGACCTGGCGGACACCATGGTCAAGACCC				
MtugInA2	(479)	CG-GTGCACGACTCCGGCTTGAACCTTGGCGGCCACCGGATGGATGCC				
MtugInA3	(488)	TG-GTGGAGACGGGGTTCG-TCCGGGATGTCAACGCCCGGCAA				
MtugInA4	(545)	CATCCCTGGGGATGGAGCCGTTG-CTGGGGACATCCGGTTGGTA				
MtugInA1	(569)	CC-CCCAACGACCAAATACGTGACCTGGCGACAAAGATGCAACCAACC				
Consensus	(601)	CA CCCTACGACCAA CGGT GAC TGCGCGATGACATGGT GGCAACC				
	651	700				
2247	(617)	TCGCAGCTTCCGGCTTCCTCTTGGCGTTTCCACCAAGAAGTCGG-----T				
13032	(617)	TCGCAGCTTCCGGCTTCCTCTTGGCGTTTCCACCAAGAAGTCGG-----T				
CEFgInA1	(617)	TCGCAGCTTCCGGCTTCCTCTTGGCGTTTCCACCAAGAAGTCGG-----T				
CEFgInA2	(626)	TGGCGGAGATCGGGTTCACCGTGGAGCGTTCCACCAAGAAGTCGG-----T				
MtugInA2	(527)	TGGAATTCTGGGCACTCGGTTGGAGGTTCAACCACTACCGAAGGGG-----A				
MtugInA3	(533)	CGGCAG-CAGGCACTCCATACTGGAGCAGTCCCACTCCGAATACGG-----I				
MtugInA4	(590)	TGGCGGGTGGGGCTGGGATCGAGGCTGGAGGGTCAAGGCGGAATGAAA-----C				
MtugInA1	(617)	TGATCAACTCCGGCTTCATCCTGGAGAAGGGCCACCAACGAGGTGGGCAGC				
Consensus	(651)	TGGCAG CCGGCTTC C CTGGAGCGTTCCACCAACGAGTCGG T				
	701	750				
2247	(664)	GGCGGACAGCAGGAATCAACTACCGCTCAACACCAATGCTCCACGCCGC				
13032	(664)	GGCGGACAGCAGGAATCAACTACCGCTCAACACCAATGCTCCACGCCGC				
CEFgInA1	(664)	GGCGGCCAGCAGGAGATCAACTACCGCTCAACACCCCTCTGCACGCCAGC				
CEFgInA2	(676)	GGTGGTCAAGCAGGAGATCAACTACCGCTCAACACCCCTCTGCACGCCAGC				
MtugInA2	(574)	CCCGGCCAGCAGGAGATCAACTACCGCTGGCGGCTGGCGACCGCTGGCGATGGC				
MtugInA3	(577)	GCCAAACCAATCGAGATCTGGTTAGCGCCGAGCCCGGGCGCAGCGGGCAGC				
MtugInA4	(637)	ATGGGGCAGCAGGAGATGGGTTCTGGTTAGACGAGGGCTGGTACACCTG				
MtugInA1	(667)	GGCGGACAGGCCAGGAGATCAACTACCGATCAACCTGGCTGGACGCCGG				
Consensus	(701)	GGCGGCCAGCAGGAGATCAACTACCG TTCAACACCCCTGCTGCACGC GC				
	751	800				
2247	(714)	AGATGATAATCCAGACCTCAAGTACATCATCAAGAACACCGCTGGCTCC				
13032	(714)	AGATGATAATCCAGACCTCAAGTACATCATCAAGAACACCGCTGGCTCC				

CEFgInA1	(714)	CGATGACATTAGACCTTCAAGTACATCGTGAAGAACACCGCAGCCCTGC	
CEFgInA2	(726)	CGATGACCTCCAGACCTTCAAGTACGGTGAAAGAACACCGCGAAGGCCG	
MtugInA2	(624)	TGACAACGTGATGACCTTCGGCTACGTCATCAAAGAACACTCGCGTGAAAG	
MtugInA3	(627)	CGATCAGGTTGGTCTGACCCGGCTCATCATCGGCCGTACCGCCGGCCGGC	
MtugInA4	(687)	CGACAAACCATGCGATCTACAAGAACGGCGCAAGGAAATCGCCGACAGG	
MtugInA1	(717)	CGACGACATGCGAGTTGACAAGTACATCATCAAAGAACACCGCCTCGCAGA	
Consensus	(751)	CGATGACAT CAGACCTTCAAGTACATCATCAAAGAACACCGC CGCC GC	
		801	850
2247	(764)	ACGGCAAGGCTGCAACCTTCATGCCAAGCCCTGGCGACAAACGGT	
13032	(764)	ACGGCAAGGCTGCAACCTTCATGCCAAGCCCTGGCGACAAACGGT	
CEFgInA1	(764)	ACGGCAAGGCTGCCAACCTTCATGCCAAGCCCTGGCGACAAACGGC	
CEFgInA2	(776)	TGGTAAATCCGCCAACCTTCATGCCAAGCCCTGGCGACAAACGGT	
MtugInA2	(674)	AGGGCGCCCGGGCTCGTTCATGCCAAGGCCATCGGCCAGCACCCGGC	
MtugInA3	(677)	ACGGGTTACGGCTGAGGCTATGCCAGCCCTCGCCGGAAAGTATCGGA	
MtugInA4	(737)	ACGGCAAGAGCCTAACGTTCATGCCGAAATACGATGAAACCGGAAGGT	
MtugInA1	(767)	ACGGCAAAACGGCTACGTTCATGCCAAGCCCTGTTGGCGACAAACGGG	
Consensus	(801)	ACGGCAAG C GC ACCTTCATGCCAAGCCACTGGCTGG GACAACGGT	
		851	900
2247	(814)	TCGGGCATGCACCGCTACCCAGTCCCTGGAGG—ACGGCAAGCCACT	
13032	(814)	TCGGGCATGCACCGCTACCCAGTCCCTGGAGG—ACGGCAAGCCACT	
CEFgInA1	(814)	TCGGGCATGCACGCCAACAGTCCTGTGGAGG—ACGGCAAGCCACT	
CEFgInA2	(826)	TCGGGCATGCACATCCACCCAGTCGCTGTGGAGG—ACGGCAAGCCCT	
MtugInA2	(724)	TGGCGATGGACACCCACATGAGCCTGTTGGAGGTAATGCAACGGGT	
MtugInA3	(727)	TCCGGTGCCTACCAACACTCTCGCTGACTATGTCGGAGGGAT—GCT	
MtugInA4	(784)	AATAGGTGTCAATCCATGTCCTCGCTGCCACGGATGGCTCCGGGT	
MtugInA1	(817)	TCCGGCATGCACTGTCACTAGTCGCTGTGGAGG—ACGGGGGCCCGCT	
Consensus	(851)	TCCGGCATGCAC CCCACCAAGTCGCTGTGGAGG ACGGCAAGCCGCT	
		901	950
2247	(861)	CTTCCACGATGA GTTCCCCTACGAGGCCCTGTCGACATCGCCCCCTAC	
13032	(861)	CTTCCACGATGA GTTCCCCTACGAGGCCCTGTCGACATCGCCCCCTAC	
CEFgInA1	(861)	CTTCCACGACGA GTTCCCCTACGCCGCCCTGTCGACATCGCCCCCTAC	
CEFgInA2	(873)	CTTCCATGATGA GGCCCCCTATGCCAACCTGTGGAGATGGCCCGTCAC	
MtugInA2	(774)	CCACAGCCGCTGATGATGCCCT—GCAG—CTGTCGGAGGGTAAACCG	
MtugInA3	(774)	GTTCTCCGGTGG—GACTGGAGCACCTGGCAAGACCTGGCCGGGAGGCC	
MtugInA4	(834)	GTTTGGCACGTAACGGGCCGACGG—CATGTCGTCGATGTTCCGCAGC	
MtugInA1	(864)	GATGTACGACGA GACGGGTTAUGGGGTCTGTCGGACACGGCCGTCAT	
Consensus	(901)	CTTCCACGATGA GACGGGCTACGC GGCCCTGTCGGACATGGCCCG TAC	
		951	1000
2247	(910)	TACATCGGGCGCATCCTGCACCAACCGCAGGGCGTGTCTGGCGTT—CACCA	
13032	(910)	TACATCGGGCGCATCCTGCACCAACCGCAGGGCGTGTCTGGCGTT—CACCA	
CEFgInA1	(910)	TACATCGGTGGCATCCTGCACCAACCGCAGGGCTGGCTCTGGCGTT—CACCA	
CEFgInA2	(922)	TATGTCGGTGGCTGCTGCTAACGCACTCCCCCGCCGGTGTGGCTTT—CACCA	
MtugInA2	(820)	TTCATCGCCGGGATCCTGGAGCACGCTTGGAGATCACGGCGGT—CACCA	
MtugInA3	(823)	GCGGTTGGCACGGAGTGCTTC—GCGGACTAACCGACGCCAACGATCCTGT	
MtugInA4	(883)	TTCGTCGGCGGCCAGTGG—CCACGTTGGCGAAATCACGCTGTGCTATG	
MtugInA1	(913)	TACATCGGGCGGCTGTTAACCAACCGCAGGGCTGGCTGCTGGCCCT—CACCA	
Consensus	(951)	TACATCGGGCGCATGCTGCACCAACCGC GGCCGGT CTGGCGTT CACCA	
		1001	1050
2247	(959)	ACGGAAACCCCTGAACCTCCTACCAACCGTCTGGT TCCAGGCTTCGAGGGCTCCA	
13032	(959)	ACGGAAACCCCTGAACCTCCTACCAACCGTCTGGT TCCAGGCTTCGAGGGCTCCA	
CEFgInA1	(959)	ACCCGACCCCTGAACCTCCTACCAACCGTCTGGT TCCAGGCTTCGAGGGCCCC	

CEFglnA2	(971)	ACCCGACCCCTGAATTCCCTACAACCGTCTGGTGCCTGGGTTTCGAGGGCCCC
MtuglnA2	(869)	ATCAGTGGGTCAACTCTTACAAGCGCTGGTGCAGGGCGCGAAAGGGCCC
MtuglnA3	(872)	GGGGATCGATCGTGCCGGTCTGGAAATGCCAACCGGTAACCTGGCCCGGA
MtuglnA4	(932)	CGCCGACCATTAACCTCTACAAGCGATTTGCCGATAAGCTTCGGGCCG
MtuglnA1	(962)	ACCCGACGGTGAACCTCTACAAGCGCTGGTCCCCGGTTACGAGGGCCCC
Consensus	(1001)	ACCCGACCCCTGAACCTCTACCAGGGCTGGTCCGGTCCGGTCCGGTCCGGT
	1051	1100
2247	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTCTCCGCTGCTGTCCGATATCCC
13032	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTCTCCGCTGCTGTCCGATATCCC
CEFglnA1	(1009)	ATCAACCTGGTCTACTCCAGCGCAACCGTCTCCGCGGCCGTGCGATATCCC
CEFglnA2	(1021)	GIGAGCCCTGGCGTATTCGAGCGAGAACCGUTCCGCCGCCATCCCGATTTCC
MtuglnA2	(919)	ACGGCCGCCGCTCGTGGGGGGCCAACCGATCCGCCCTAGTGGGGGTGGC
MtuglnA3	(922)	ATCTATGATGCTGGGGTACCGAAACCGGAAAGCGGCCGTGGATTCGT
MtuglnA4	(982)	ACGGCGCTGGCTGGGGCTGGACAAATCCCACTGCCGGCTGGGTG--
MtuglnA1	(1012)	ATCAACCTGGTCTATAGCCAGCGCAACCGTCTGGCATGCGTGGCATCCC
Consensus	(1051)	ATCAACCTGGTGTATGAGCGCAACCGTCTGGCATGCGTGGCATCCC
	1101	1150
2247	(1059)	AAT---CACCGGATCCAACCCAAAGGCAAAGGCCATCGAATTCCGGCGC
13032	(1059)	AAT---CACCGGATCCAACCCGAAGGCCAAGGCCATCGAATTCCGGCGC
CEFglnA1	(1059)	GAT---CACCGGTTCCAACCCGAAGGCCAAGGCCATCGAGTTCCGGCGC
CEFglnA2	(1071)	GGC---CACCGGCTCCAACCCGAAGGCCAAGGCCATCGAGTTCCGGCACCC
MtuglnA2	(969)	GATGTAACCGCCGACAAGACCTCTCGCCGGGGTCCAAAGTACCGCAGCC
MtuglnA3	(972)	CAAGGGCGGGGCTGGCAGCGGTACGGCGGAACGIGGGAGGIGAAGGTG
MtuglnA4	(1030)	GITGGCCACGGG---CAAAACAT---C---CGGGTGGAAATGCCGGGTTC
MtuglnA1	(1062)	GAT---CACCGGCAAGCAACCGGAAGGCCAAGGCCATGGAGTTCCGAGCC
Consensus	(1101)	GAT CACCGG CCAACCGGAAGGC AAGGCCATCGAGTTCCGGCGCC
	1151	1200
2247	(1106)	CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAGGGATGATGATGGCC
13032	(1106)	CAGACCOATCAGGCAACCCATACCTGGGCTTCGCAGGGATGATGATGGCC
CEFglnA1	(1106)	CGGACCCATCCGGCAACCCCTACCTGGGCTTCGCAGGGATGATGATGGCC
CEFglnA2	(1118)	CGGACCCCTCGGGTAACCCCTACCTGGGCTTCACCGGGCTCGATGATGGCC
MtuglnA2	(1019)	CTGATTGGCGTGCATCCCTATCTGACATTGCCGCTGCTGCTGGCCGCG
MtuglnA3	(1022)	TGACCCGTCGGCCAACCGGTATCTCGCGTCGGCGCGATCTCGGACTG
MtuglnA4	(1070)	CGGGCGGTGATGTCACCACTGACCTGGGCTGGCGGCTCICATGCTGGA
MtuglnA1	(1109)	CCGACTCTGGCGAACCGGTATCTGGCGTCCTCGGGCATGCTGATGGCA
Consensus	(1151)	C GACCC TCGGGCAACCC TACCTGGGCTTCGC GGGATGATGATGGC
	1201	1250
2247	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACAGGCTCCAGTGGACAA
13032	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACAGGCTCCAGTGGACAA
CEFglnA1	(1156)	GGCCTGGACGGCATCCGCAACCGCATCGAGCCACAGGCTCCAGTGGACAA
CEFglnA2	(1168)	GGCCTGGACGGCATCCGCAACCGCATCGAGCCACAGGCTCCAGTGGACAA
MtuglnA2	(1069)	GGATTCGGGGGTAGAGAAGGGTACGTGCTGGGCGCGCAGGCCGAGGA
MtuglnA3	(1072)	GCACTCGACGGCATGAAGACCAAGCGGTGTTGCCGTCGGAAACGACCGT
MtuglnA4	(1120)	GGGTGTTACGGTATCGACGGGCTTCAGCTGCCAGGCCCTGTGTCGG
MtuglnA1	(1159)	GGCCTGGACGGTATCAAGAACAGATCGAGCCGCAGGCCGCTGACAA
Consensus	(1201)	GGCCTGGACGGTATCAAGAACCGCATCGAGCCGCACCGGCC GTGGACAA
	1251	1300
2247	(1206)	GGACCTCTACGAACGGCATGGCAGGGAGGCTGCATCAT-----TCCAC
13032	(1206)	GGACCTCTACGAACGGCATGGCAGGGAGGCTGCATCAT-----TCCAC
CEFglnA1	(1206)	GGACCTCTACGAGCTCCACCGGAGGGAGGCCCTCAT-----CCCGC
CEFglnA2	(1218)	GGACCTCTATGAGCCTCCCGGAGGGAGGCCAAGG-----CGCG

Mtu	lnA2	(1119)	CAACGTATGGGACCTCACACCCGAGGAACGCCGAGGGATGGGTACCGAG	
Mtu	lnA3	(1122)	AGACCCGACACAGCTGTCGACGTGGATCGTGACCGTGCCGGCATTCGTG	
Mtu	lnA4	(1170)	CAAGG-CCT-ACC-AAGCGCCGATGT-CGAAC	
Mtu	lnA1	(1209)	GGATCTCTACGGAGCTCCGGCGGAAGAGGGCGCGAGTAT-CCCAC	
Consensus		(1251)	GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT CCCAC	
		1301		1350
2247		(1250)	AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCCTGAGGAAGACACC	
13032		(1250)	AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCCTGAGGAAGACACC	
CEFg	lnA1	(1250)	AGGCACCGACCTCCCTGGAAGGCATCCCTGAAGGGCCTGAGGGACTCC	
CEFg	lnA2	(1262)	AGGCCCGAACCTCACTGGAACAGGCGCTGAAGGGCCTGGAGGGAGAACAC	
Mtu	lnA2	(1169)	AATTGCGGTCAGTTGGATAGTGGCTTCGGCCTGGAGGCCTCC	
Mtu	lnA3	(1172)	GACTTGTGCGATCAGGCGGATGCAATTCCTGTACTGGATAG-TTC	
Mtu	lnA4	(1199)	GGCTGGGGGTAACTGCTGGCGAAGCCGCGGTGCTGTTCGAGGA-TTCT	
Mtu	lnA1	(1253)	AGACTCCGACCCAGCTGCAAGATGTGATCGACCGCTCGAGGCCGACAC	
Consensus		(1301)	AGGC CGCACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC	
		1351		1400
2247		(1300)	GACTTCCTCACCGAGCTGACGTCTTCACCGAGGATCTCATCGA-GGGT	
13032		(1300)	GACTTCCTCACCGAGCTGACGTCTTCACCGAGGATCTCATCGA-GGGT	
CEFg	lnA1	(1300)	GACTTCCTCACCGAGCTGACGTGTTACCGAGGACCTTCATCGA-GGCCT	
CEFg	lnA2	(1312)	GAGTTCTCACCGAGGGTGACGTGTTACCGATGATCTCATCGA-GGCCT	
Mtu	lnA2	(1216)	GAACCTCGTGGGGAG-GCCCTGGGGAGCACGTTTUGA-CTTTT	
Mtu	lnA3	(1218)	GAAACTGCTTGGGTG-CATCCCTGGGGATCCCGTGGTAGATGGCGT	
Mtu	lnA4	(1246)	GCGCTGGTGGCGAG-GCGTACGGGAGGATGTTGTCGC-GCACT	
Mtu	lnA1	(1303)	GAATACCTCACCGAAGGAGGGTGTTACAAAAGACACTGATCGA-GACGT	
Consensus		(1351)	GA TTCTCACCGAG GACCTGTTACCGAGGATCTCATCGA GGGT	
		1401		1450
2247		(1349)	ACATCCCACTACAAGTAG-GACAACGAGATCTCCCCAGT-CGGCTGCGC	
13032		(1349)	ACATCCCACTACAAGTAG-GACAACGAGATCTCCCCAGT-CGGCTGCGC	
CEFg	lnA1	(1349)	ACATCCCACTACAAGTAG-GACAACGAGATCCCCGGT-CGGCTGCGC	
CEFg	lnA2	(1361)	ATGTGGCTTACAAGCAT-GAACATGAGATCACCCCTGACCGTCTGGC	
Mtu	lnA2	(1259)	TCTTGGCGACAAGCGACCGAGTGGGGCAACTACCGCAGCCACG-CACG	
Mtu	lnA3	(1263)	GGTCGGGGTACGCCAT-TAGAGCATGAGCGCTAAC-GGTGACCTCGAT	
Mtu	lnA4	(1289)	ACCTGAAACACGCCGCTGTGGAGCTGGCGCGTGAACGCCGGICA-	
Mtu	lnA1	(1352)	GGATCAGTTCAAGCGC-GAAAACGAGATCGACCCGGTCAACACACGG	
Consensus		(1401)	ACATGCACTACAAGCGC GA AACGAGATCTCCCC GT CGCCTGCGC	
		1451		1495
2247		(1396)	CCACCCCGCAGGAATCGAATTGTACTTCGACTGC	
13032		(1396)	CCACCCCGCAGGAATCGAATTGTACTTCGACTGCTAA	
CEFg	lnA1	(1396)	CCACCCCGCAGGAATCGAATTGTACTTCGACTGCTAA	
CEFg	lnA2	(1408)	CCACCCGCTCTGGATTCGAGCTGTACTACGACTGCTAG	
Mtu	lnA2	(1309)	CCATAACGAGCTGCGCACCTACCTGTGCGCTGTAG	
Mtu	lnA3	(1309)	CCTGGCGAGCTGGCCGACAAGTCCGGATGGCTTGGAGTGTGTAACG	
Mtu	lnA4	(1337)	CCGATTGGGAGAGGATACGTGGATITGAGCGCCCTCTAG	
Mtu	lnA1	(1399)	CCGCATCCCTACGAAATCGCGCTGTACTACGACGTTAA	
Consensus		(1451)	CC ACCCCCGCAGGAATCGAGCTGTACTTCGACTGCTA	

2247 : *B. flavum* ATCC14067

13032: *C. glutamicum* ATCC13032

CEF: *C. efficiens* YS314

Mtu: *Mycobacterium tuberculosis* H37RV